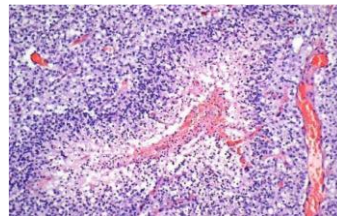


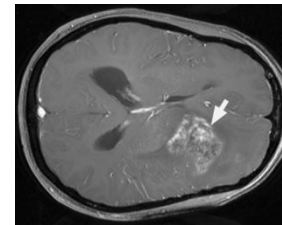
# Overview of Web-based Tools to Support Imaging Based In Silico Research

David A Gutman MD PHD  
9/26/2011

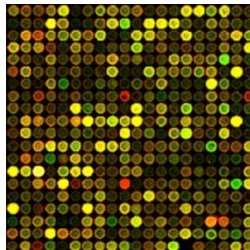
*histology*



*radiology*



*molecular*



*clinical/pathology*

	A	B	C	D	E
1	Age at Dx	Gender	Survival	Disease	
2	30-34	F	>60M	OLIGODENDRO	
3	50-54	M	--	GBM	
4	50-54	M	--	GBM	
5	50-54	F	30-36M	GBM	
6	20-24	M	--	UNKNOWN	
7	65-69	M	12-18M	UNKNOWN	
8	55-59	F	--	ASTROCYTOMA	

**Integrated  
Analysis**

## Brief Overview

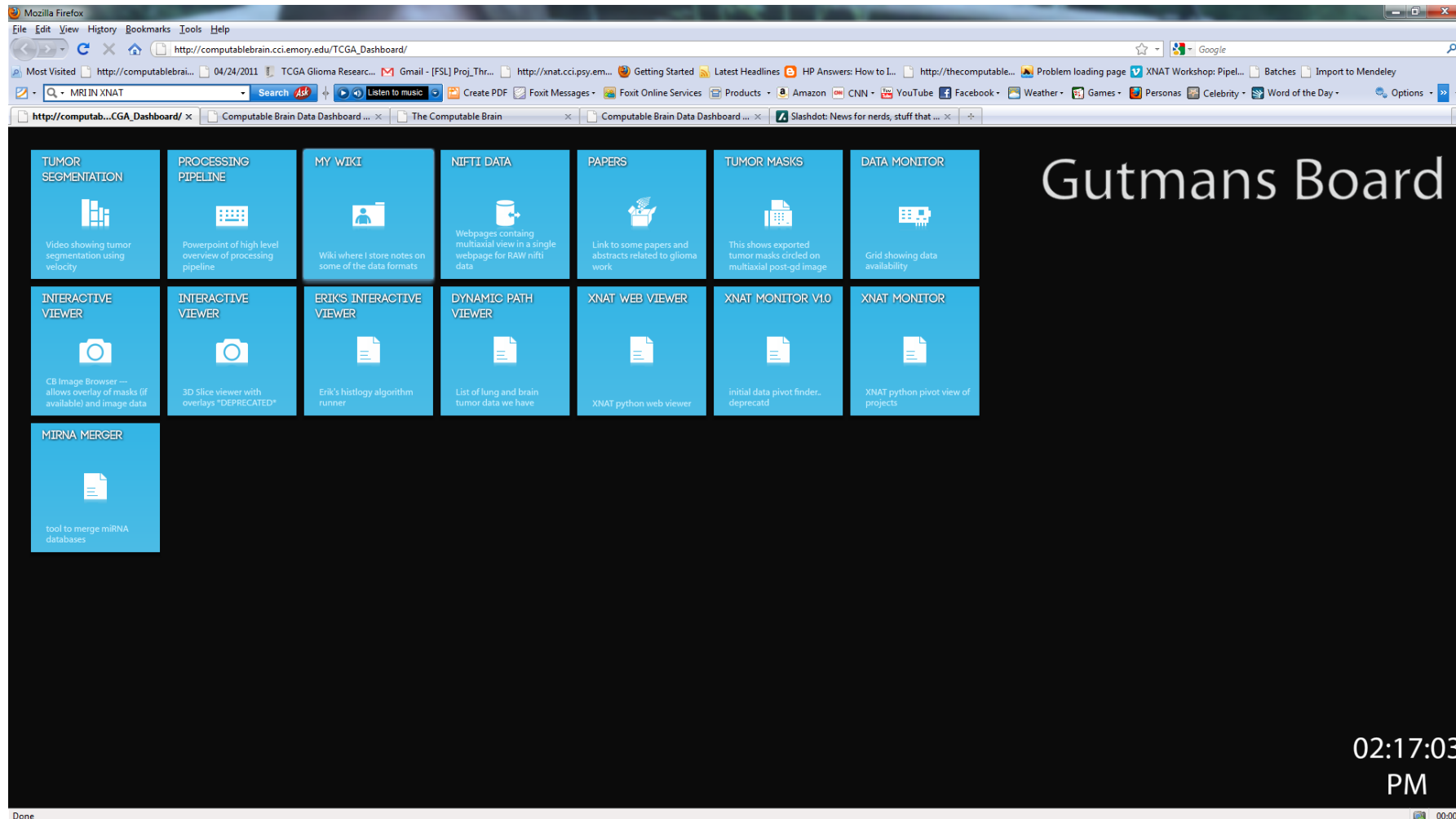
- TCGA Portal is very OMICs focused
- To support our *in silico* work we have developed a number of web-based tools to support informatics integration as well as visualization of results
- Prototypes roughly fall into 3 domains
  - Radiology workflow tools
  - Portals to find common data sets across imaging pipelines
  - Pathology image analysis work/ QA


















Apps are available  
online... Brief  
descriptions on  
following slides

[http://computablebrain.cci.emory.edu/TCGA\\_Dashboard/](http://computablebrain.cci.emory.edu/TCGA_Dashboard/)

Has a general base link... number of active sites are here



**Gutmans Board**

<b>TUMOR SEGMENTATION</b>  Video showing tumor segmentation using velocity	<b>PROCESSING PIPELINE</b>  Powerpoint of high level overview of processing pipeline	<b>MY WIKI</b>  Wiki where I store notes on some of the data formats	<b>NIFTI DATA</b>  Webpages containing multiaxial view in a single webpage for RAW nifti data	<b>PAPERS</b>  Link to some papers and abstracts related to glioma work	<b>TUMOR MASKS</b>  This shows exported tumor masks circled on multiaxial post-gd image	<b>DATA MONITOR</b>  Grid showing data availability
<b>INTERACTIVE VIEWER</b>  CB Image Browser — allows overlay of masks (if available) and image data	<b>INTERACTIVE VIEWER</b>  3D Slice viewer with overlays *DEPRECATED*	<b>ERIK'S INTERACTIVE VIEWER</b>  Erik's histology algorithm runner	<b>DYNAMIC PATH VIEWER</b>  List of lung and brain tumor data we have	<b>XNAT WEB VIEWER</b>  XNAT python web viewer	<b>XNAT MONITOR V1.0</b>  initial data pivot finder. deprecated	<b>XNAT MONITOR</b>  XNAT python pivot view of projects
<b>MIRNA MERGER</b>  tool to merge miRNA databases						

02:17:03  
PM

[http://thecomputablebrain.com/DASHBOARD/DASHBOARD\\_IMAGES/](http://thecomputablebrain.com/DASHBOARD/DASHBOARD_IMAGES/)

**Can quickly view summary images of data belonging to a given image type (i.e. see all the images labeled AXIAL T1 PRE GD)**



[http://trauma-computernode1.psychiatry.emory.edu/COMPUTABLE\\_BRAIN/DASHBOARD/PHP\\_CODE/](http://trauma-computernode1.psychiatry.emory.edu/COMPUTABLE_BRAIN/DASHBOARD/PHP_CODE/)

Basic Portal helps me figure out which patients have which imaging data

TCGA Glioma Data stats portal - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://trauma-computernode1.psychiatry.emory.edu/COMPUTABLE\_BRAIN/DASHBOARD/PHP\_CODE/

Most Visited http://computablebrai... 04/24/2011 TCGA Glioma Resear... Gmail - [FSL] Proj\_Thr... http://xnat.cci.psy.em... Getting Started Latest Headlines HP Answers: How to L... http://thecomputable... Problem loading page XNAT Workshop: Pipel... Batches Import to Mendeley

Search Ask Listen to music Create PDF Foxit Messages Foxit Online Services Products Amazon CNN YouTube Facebook Weather Games Personas Celebrity Word of the Day Options

http://computab...TCGA\_Dashboard/ TCGA Glioma Data stats portal Computable Brain Data Dashboard ... The Computable Brain Computable Brain Data Dashboard ... Slashdot: News for nerds, stuff that ...

## Welcome to the Computable Brain TCGA Glioma Data stats portal

Patient_ID	ADC-MAP	AXIAL-T1-POST-GD	AXIAL-T1-PRE-GD	AXIAL-T2-FLAIR	FA-MAP	POST-GD-MASK
HF2665	1	1	1	1	1	0
HF2591	1	1	1	1	1	0
HF2582	1	1	1	1	1	0
HF2579	1	1	1	0	0	0
HF2566	1	1	1	1	0	0
HF2562	1	1	1	1	1	0
HF2560	1	1	1	1	1	0
HF2548	1	1	1	1	1	0
HF2537	1	1	1	1	1	0
HF2519	1	1	1	1	0	0
HF2503	1	0	0	0	1	0
HF2501	1	1	0	1	1	0
HF2485	1	1	0	1	1	0
HF2472	1	1	1	1	1	0
HF2414	1	1	1	1	1	0
HF2371	1	1	1	1	0	0
HF2366	1	1	1	1	1	0

Done 00:00

<http://computablebrain.cci.emory.edu/Monitor/>

Previous version was static--- this one pulls data directly from local XNAT instance I have up and running

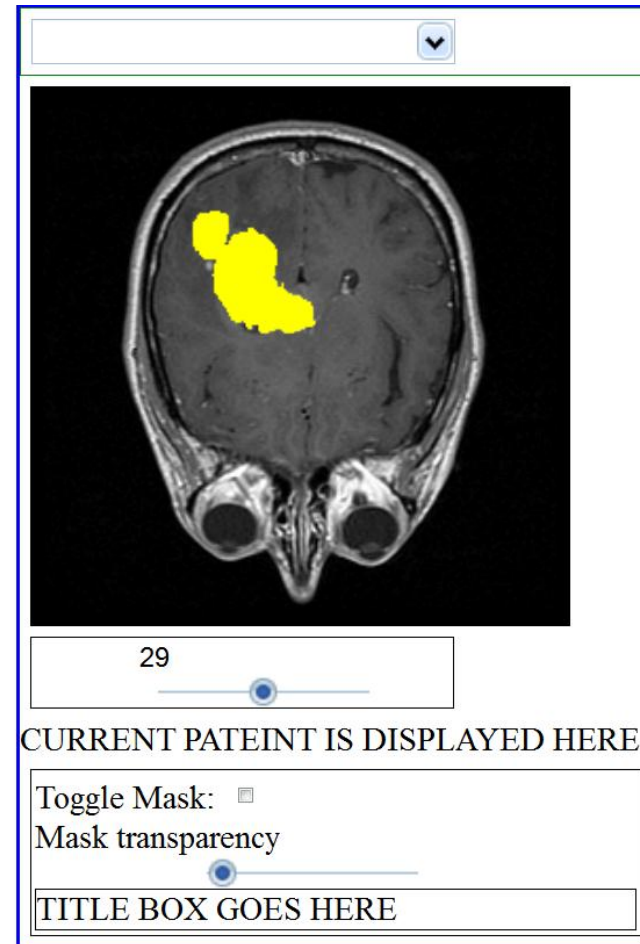
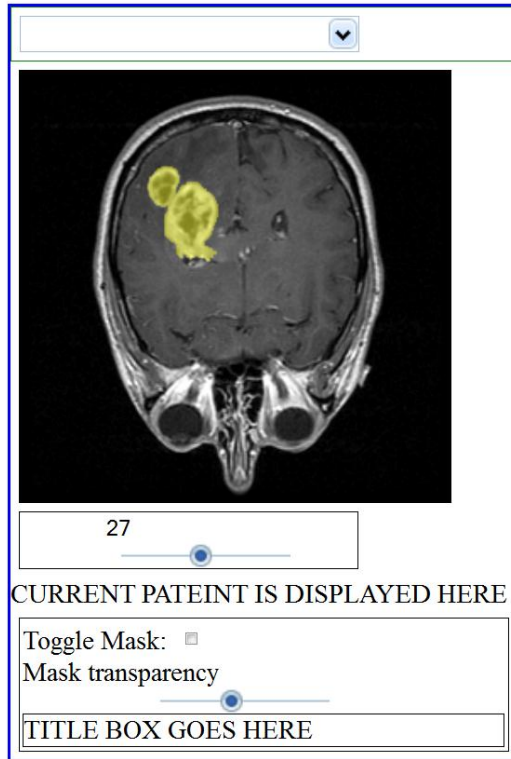
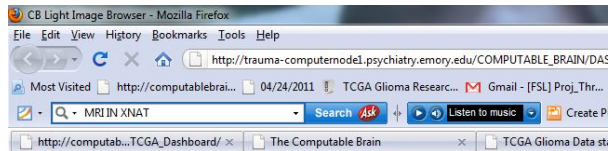
Displaying XNAT Data for

PatientID	Experiment	AXIAL T1 PRE GD		AXIAL T1 POST GD		AXIAL T2 FLAIR	
		Scan	Mask	Scan	Mask	Scan	Mask
TCGA-02-0087	CCI_XNAT_PROD_E00039	1		1		0	
TCGA-02-0086	CCI_XNAT_PROD_E00038	1		1		0	
TCGA-06-0878	CCI_XNAT_PROD_E00165	1		1		1	
	CCI_XNAT_PROD_E00166	1		1		1	
	CCI_XNAT_PROD_E00167	1		1		1	
TCGA-06-0238	CCI_XNAT_PROD_E00459	1		1		1	
TCGA-06-1801	CCI_XNAT_PROD_E00182	0		0		0	
	CCI_XNAT_PROD_E00183	0		0		0	
	CCI_XNAT_PROD_E00180	1		1		0	
	CCI_XNAT_PROD_E00187	0		0		1	
	CCI_XNAT_PROD_E00185	1		1		1	
	CCI_XNAT_PROD_E00179	0		1		0	
	CCI_XNAT_PROD_E00178	1		1		1	
	CCI_XNAT_PROD_E00177	1		1		1	
TCGA-06-1802	CCI_XNAT_PROD_E00188	1		1		1	
	CCI_XNAT_PROD_E00190	1		1		1	
	CCI_XNAT_PROD_E00192	1		1		1	
TCGA-14-0817	CCI_XNAT_PROD_E00417	0		0		0	
	CCI_XNAT_PROD_E00401	0		0		0	
TCGA-14-0813	CCI_XNAT_PROD_E00407	0		0		0	
	CCI_XNAT_PROD_E00433	0		0		0	
TCGA-14-0812							

Transferring data from computablebrain.cci.emory.edu...

Quick sanity check... part of workflow is to mask the tumor region--- below allows web based overlay of mask on base image (can adjust opacity so can see underlying structure as well)

[http://trauma-computernode1.psychiatry.emory.edu/COMPUTABLE\\_BRAIN/DASHBOARD/PHP\\_CODE/PNG\\_DEPOT/cb\\_light\\_image\\_viewer.php](http://trauma-computernode1.psychiatry.emory.edu/COMPUTABLE_BRAIN/DASHBOARD/PHP_CODE/PNG_DEPOT/cb_light_image_viewer.php)



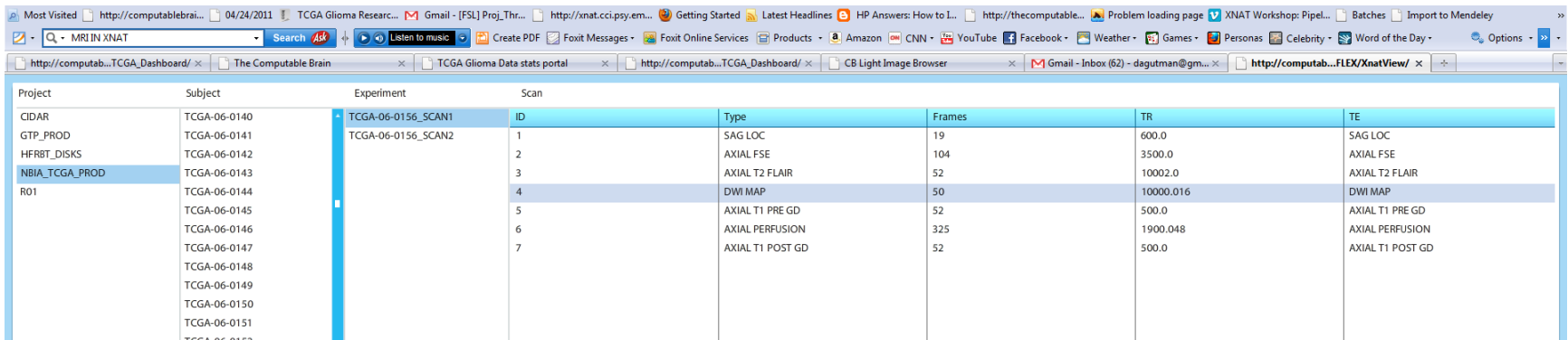
Done

Done

# Want to visualize data based on Scan Tags..

[http://computablebrain.cci.emory.edu/CB\\_FLEX/XnatView/](http://computablebrain.cci.emory.edu/CB_FLEX/XnatView/)

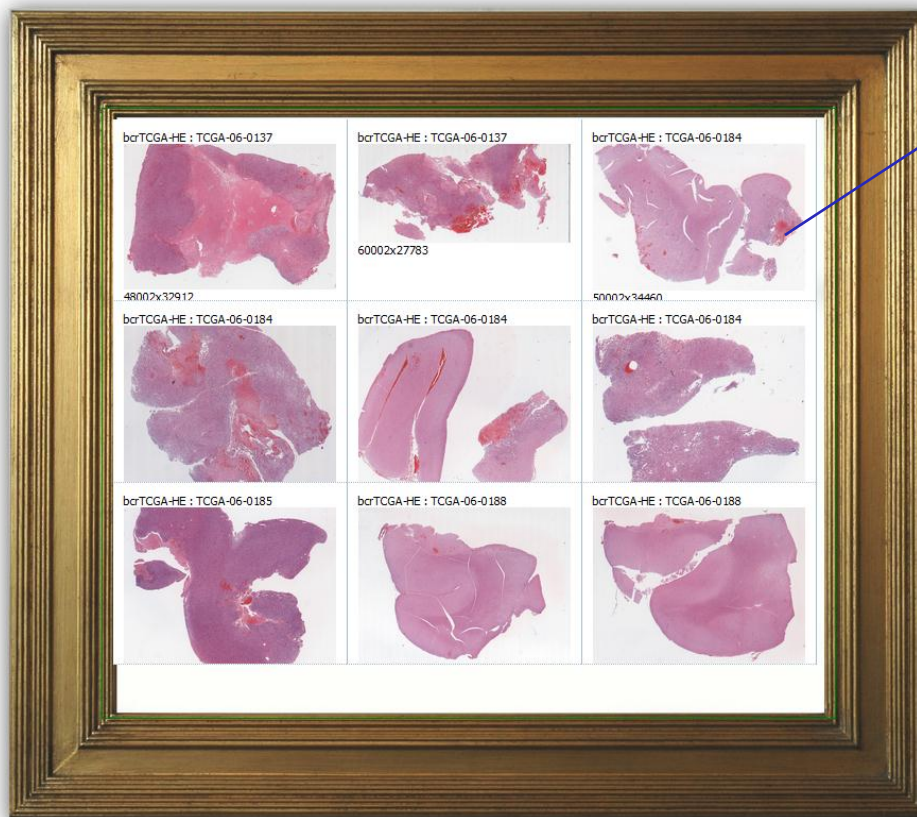
Can also see/view TR/TE/ other scan parameters to really find ideal data set;  
want to eventually integrate ability to see masks overlaid as well.. Can also pull data from other PACS if we wanted



Project	Subject	Experiment	Scan	Type	Frames	TR	TE
CIDAR	TCGA-06-0140	TCGA-06-0156_SCAN1	ID				
GTP_PROD	TCGA-06-0141	TCGA-06-0156_SCAN2	1	SAG LOC	19	600.0	SAG LOC
HFBT_DISKS	TCGA-06-0142		2	AXIAL FSE	104	3500.0	AXIAL FSE
NBIA_TCGA_PROD	TCGA-06-0143		3	AXIAL T2 FLAIR	52	10002.0	AXIAL T2 FLAIR
R01	TCGA-06-0144		4	DWI MAP	50	10000.016	DWI MAP
	TCGA-06-0145		5	AXIAL T1 PRE GD	52	500.0	AXIAL T1 PRE GD
	TCGA-06-0146		6	AXIAL PERFUSION	325	1900.048	AXIAL PERFUSION
	TCGA-06-0147		7	AXIAL T1 POST GD	52	500.0	AXIAL T1 POST GD



[http://thecomputablebrain.com/PATH\\_VIEWER/](http://thecomputablebrain.com/PATH_VIEWER/)  
Allows me to filter/find patients matching given criteria and with path



Current slide\_count 480  
 Current patient\_count 167

Sort by type [asc](#) | [desc](#)  
 Sort by name [asc](#) | [desc](#)  
 Sort by size [asc](#) | [desc](#)

[Filter by TCGA ID](#)  
[Filter by Slide group](#)  
[Clear All Filters](#)

**Note: Must click Filter by to actually filter**

**Filter By Clinical or MR Data**  
☐ MRI IN XNAT  
☐ MRI, Path and Survival and Genetics  
[Minimum Patient Age](#)  
 Filter by Verhaak Type Any  
 Filter by slide group  
 bcr TCGA Slides frozen H&E

[Clear All Filters](#)  

**Note: Must click Filter by to actually filter**

Slide Group: bcrTCGA-HE  
PT ID: TCGA-06-0137  
Gender:undefined MR\_Count:2  
KarnScore:null Verhaak  
Type:Classical  
Days to progression 487  
VASARI READS:3  
VITALSTATUS DEAD\_  
days to death 812 days to last  
followup 701

Slide Group: bcrTCGA-HE  
PT ID: TCGA-06-0184  
Gender:undefined MR\_Count:1  
KarnScore:80 Verhaak  
Type:Mesenchymal  
Days to progression null  
VASARI READS:3  
VITALSTATUS ALIVE\_HF\_C  
days to death null days to last  
followup 1228

Slide Group: bcrTCGA-HE  
PT ID: TCGA-06-0188  
Gender:undefined MR\_Count:1  
KarnScore:100 Verhaak  
Type:Neural  
Days to progression null  
VASARI READS:3  
VITALSTATUS DEAD\_  
days to death null days to last  
followup 866

**Note: Can also view patient metadata about a slide**

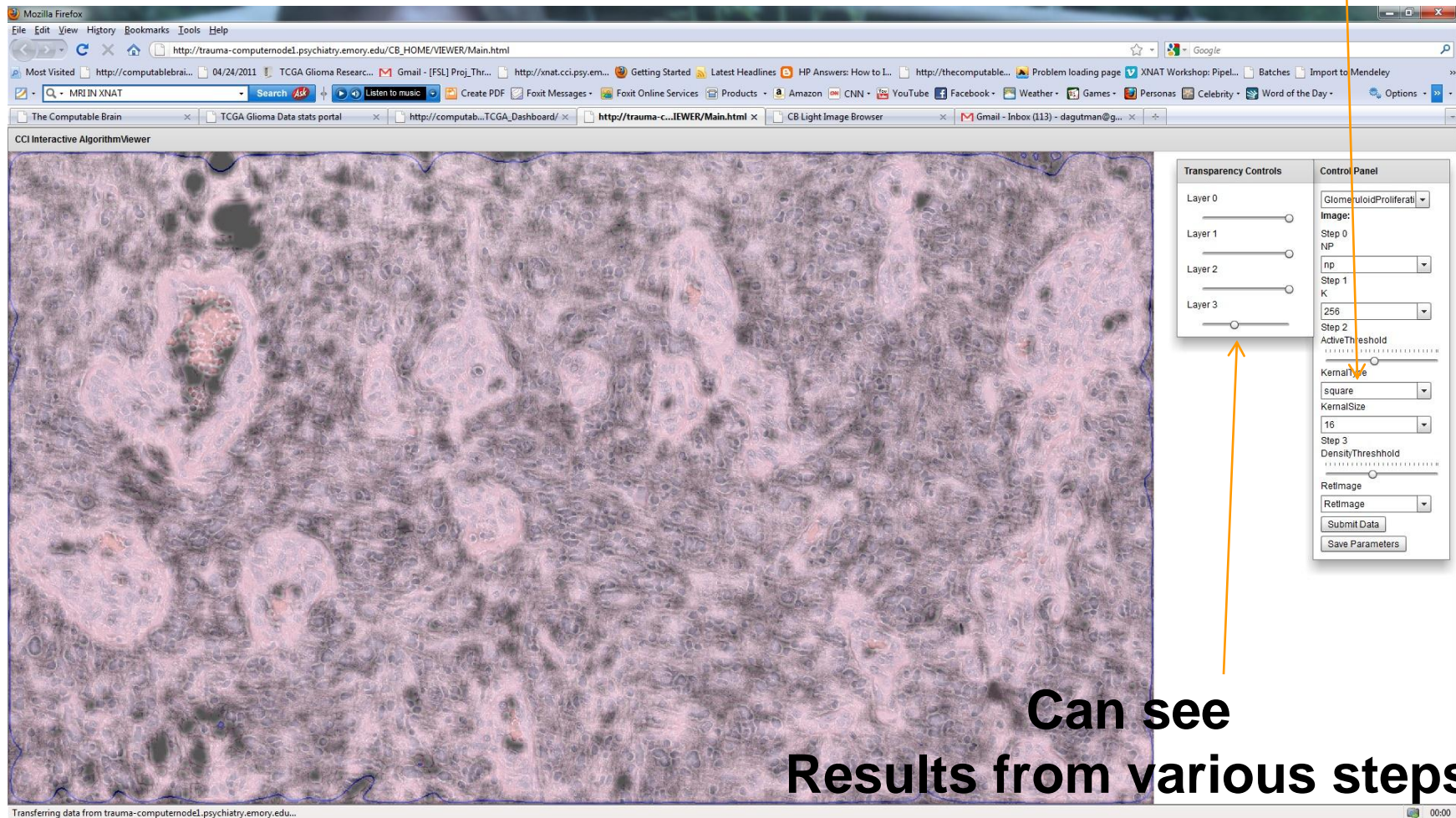
# Interactive Algorithm Runner, can run and tune

## multi-step algorithm

### Select params

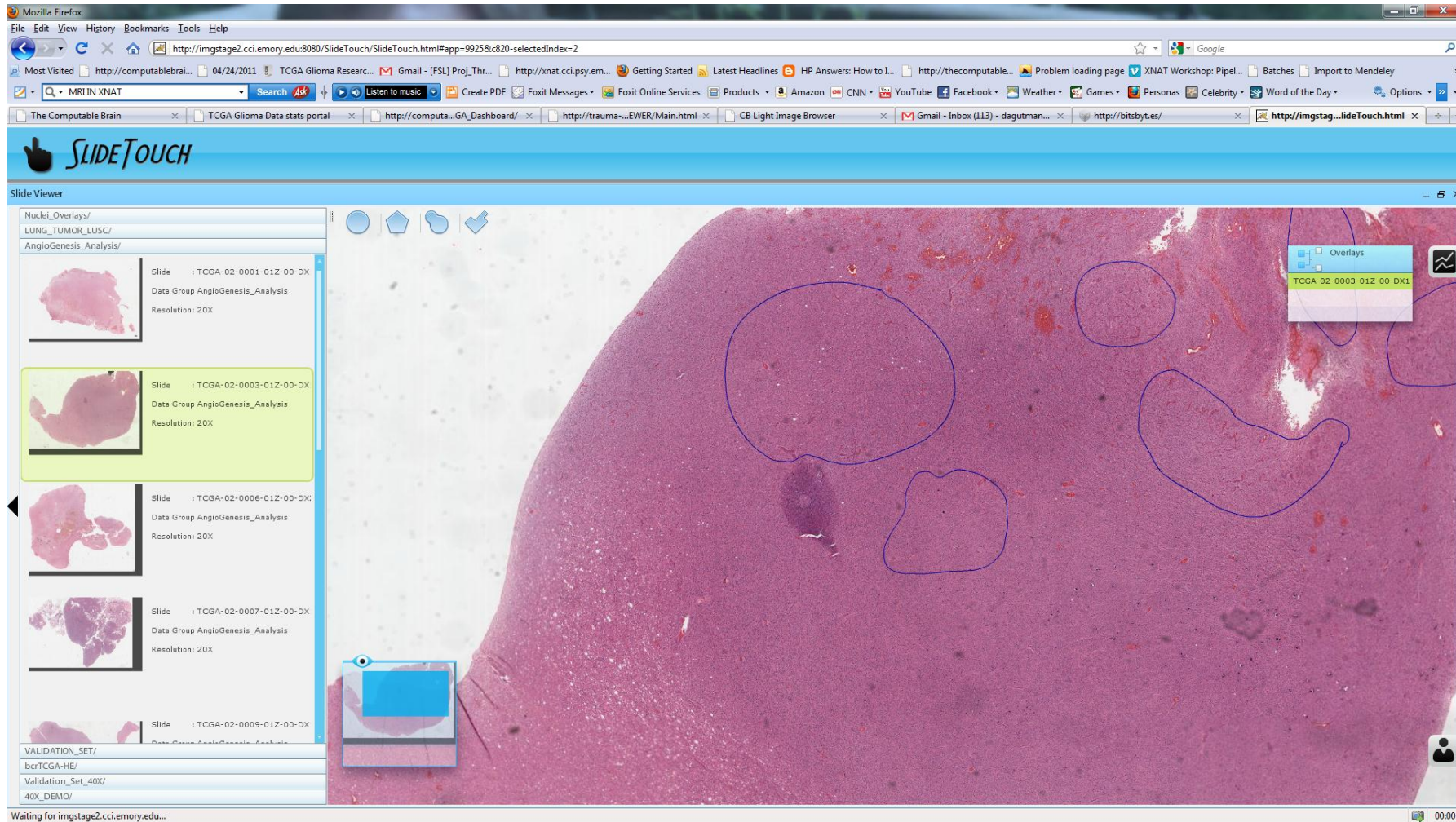
Note: This is particularly buggy

[http://trauma-computernode1.psychiatry.emory.edu/CB\\_HOME/VIEWER/Main.html](http://trauma-computernode1.psychiatry.emory.edu/CB_HOME/VIEWER/Main.html)

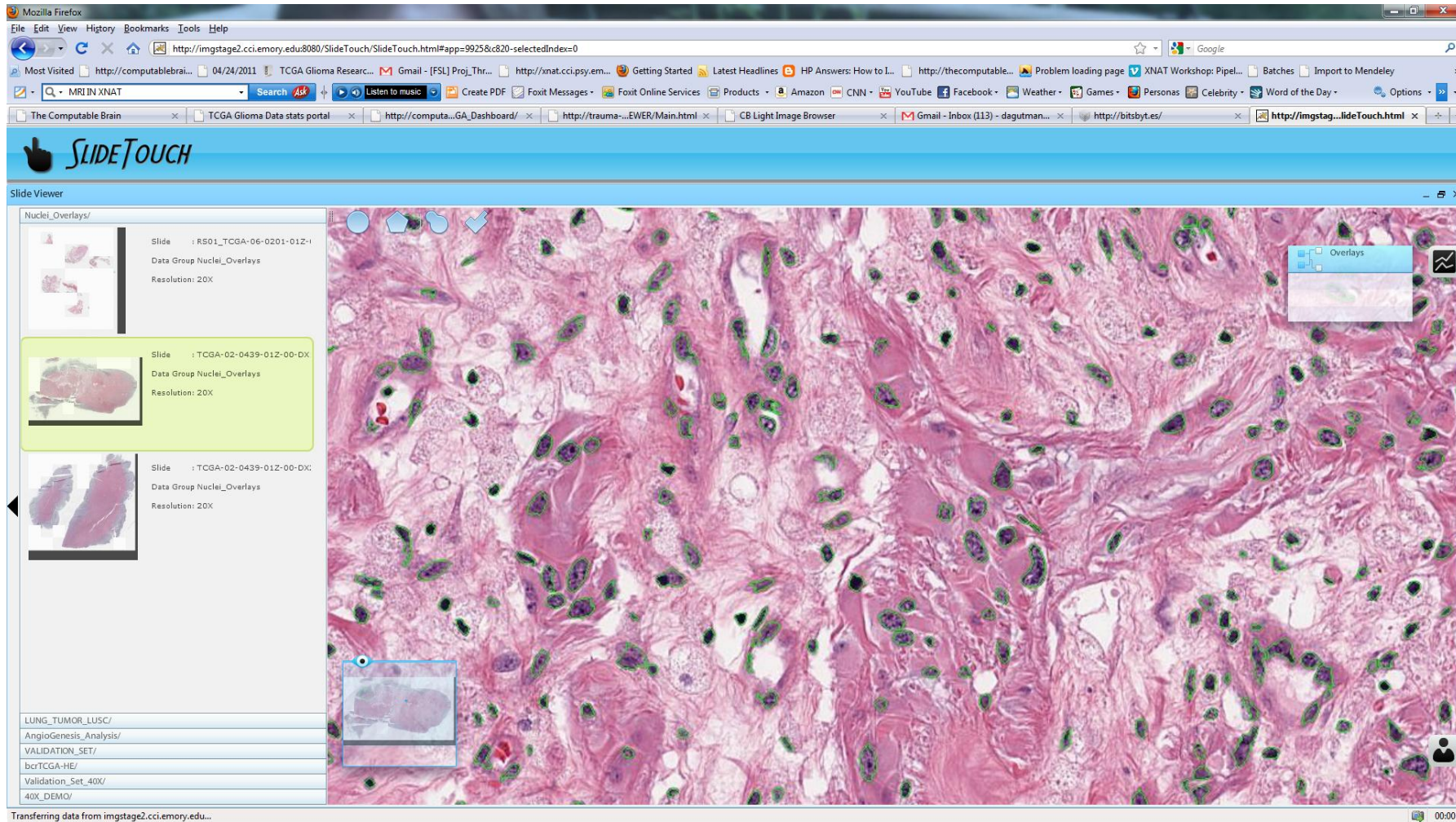


# Whole Slide Viewing app showing ROI selected

<http://imgstage2.cci.emory.edu:8080/SlideTouch/SlideTouch.html#app=9925&c820-selectedIndex=2>



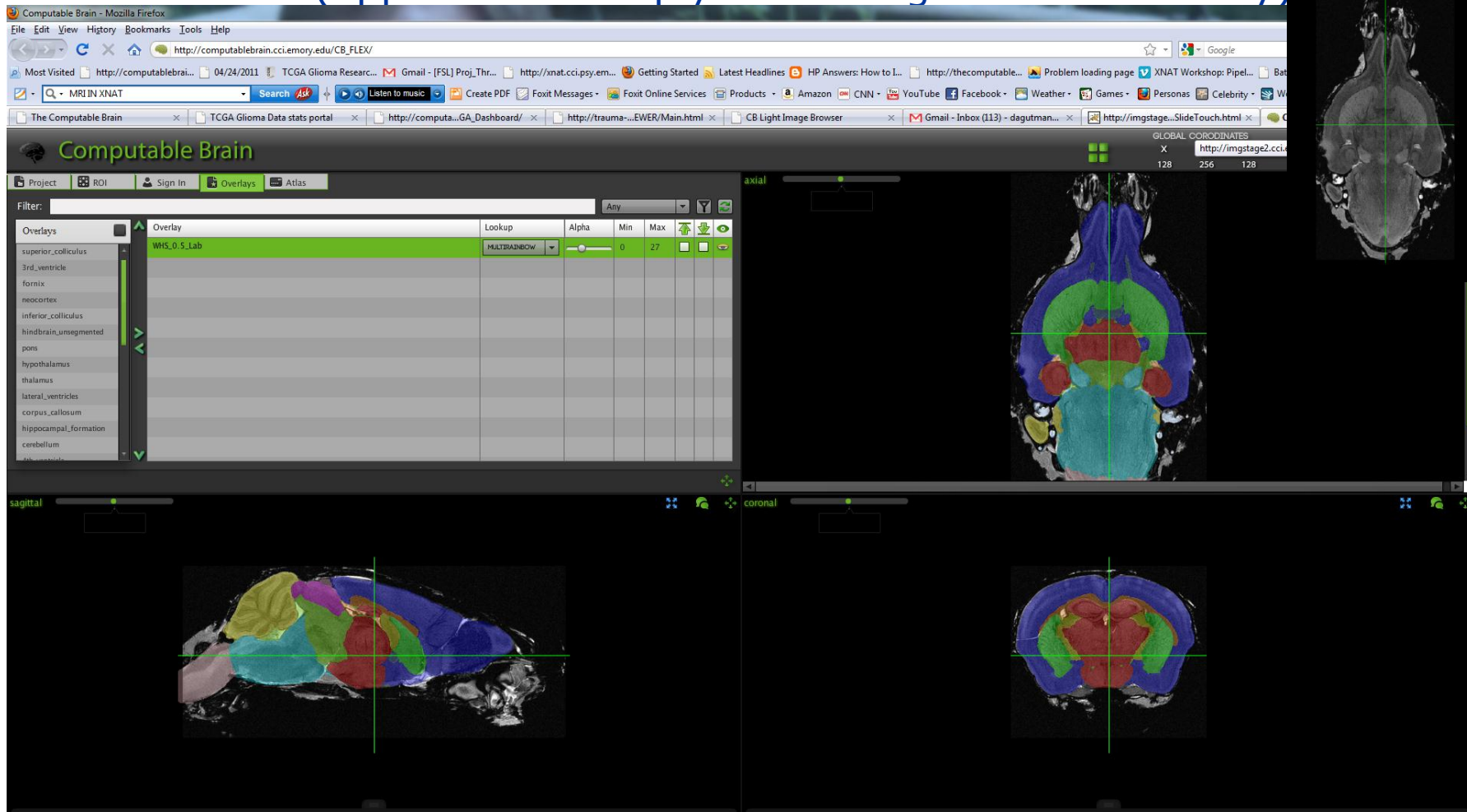
# Can also visualize analysis results (nuclei circled in green)



## Other pet project: Computable Brain

Can store imaging results online, as well as overlays/processed intermediates/etc

Showing canonical mouse atlas with atlas based ROI's shown in multicolor view (upper left is simply base image without overlay)



Also supports atlas lookups--- so can register "my" data to a reference space and do lookups to help figure out what local anatomy I am looking at



The screenshot displays the 'Computable Brain' web application interface. The top navigation bar includes 'Project', 'ROI', 'Sign In', 'Overlays', and 'Atlas'. The main content area features a table of atlases and three brain scan views (axial, sagittal, coronal).

Atlas	Atlas	Description	Intensity
	Harvard Oxford Cortical Index		
	Harvard Oxford SubCortical Index	Right Cerebral White Matter	48
		Right Cerebral Cortex	50
	JHU Tract Labels		
	JHU Tracts		

The interface also shows three brain scan views: axial, sagittal, and coronal. The axial view is currently selected and shows a cross-section of the brain. The sagittal and coronal views are also visible below it. The interface includes a search bar, a list of recent projects, and a 'Sign In' button. The bottom status bar indicates 'Transferring data from computablebrain.cci.emory.edu...' and a memory usage of '337 MB'.

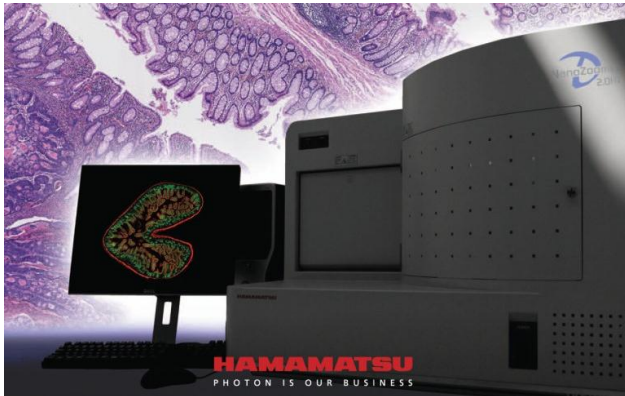


**Other slides from presentation—**

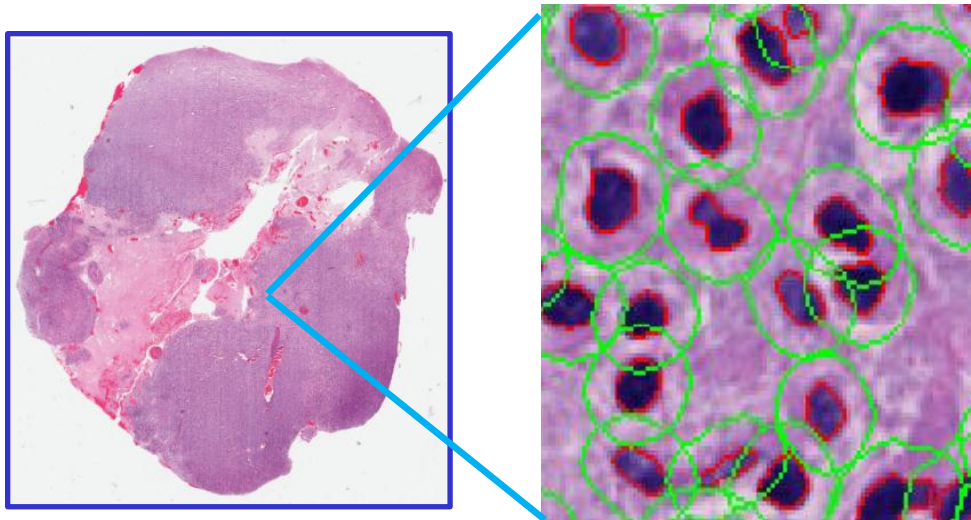
**Basically our group is interested in human generated  
And computer generation annotations and using that  
For correlative analysis of outcome... as well as building  
Tools and pipelines to assist this process.**

# Morphological subtypes study: cellular features

## Whole Slide Imaging



## Nuclei Segmentation



## Cellular Features

Nuclear Morphometry			
Nuclei Area	Nuclei Perimeter	Eccentricity	Circularity
Major Axis	Minor Axis	Extent Ratio	Fourier Shape Descriptor
Intensity Information		Texture Information	
Avg Inty	Std Inty	Entropy	Energy
Max Inty	Min Inty	Skewness	Kurtosis
Gradient Statistics			
Avg GM	Std GM	Entropy GM	Skewness GM
Energy GM	Kurtosis GM	Edge Pixel Summation	Edge Pixel Percentage

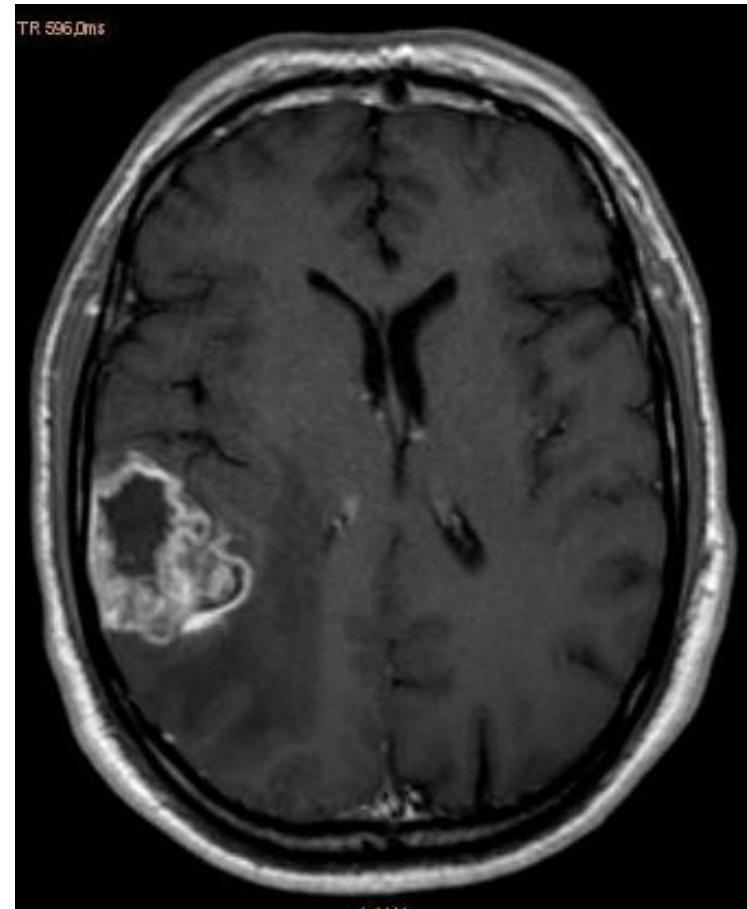
**Jun Kong**

# Mechanisms Underlying Glioma Progression

**Diagnostic Improvement**

**Molecular Classification**

**Predictors of Progression**



# TCGA and REMBRANDT Datasets

University/Project	Modality	# Patients	Total # of slides
TCGA Public Repository	20X Digital Slide	167	480
EMORY TCGA Cases	40X Digital Slide	52	195
Henry Ford TCGA Cases	40X Digital Slide	*,**70	198
Henry Ford REMBRANDT Cases	40X Digital Slides	**199	335
TJU Rembrandt Cases	40X Digital Slides	***63	230

\*Some overlap with TCGA main repository but rescanned at 40X

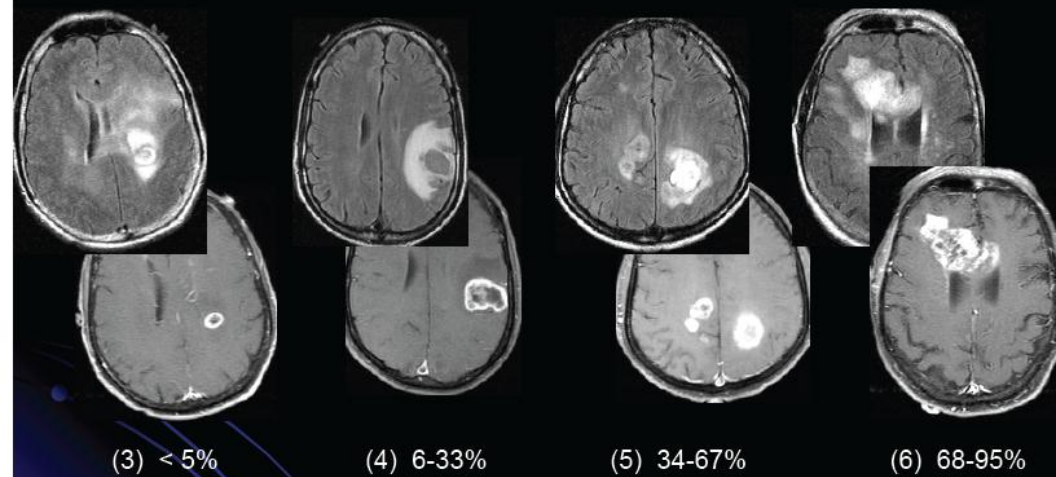
\*\* Data obtained by generosity of Lisa Scarpace/Tom Mikkelsen @ HF

\*\*\*Thanks to Adam Flanders/Mark Curtis @ TJU



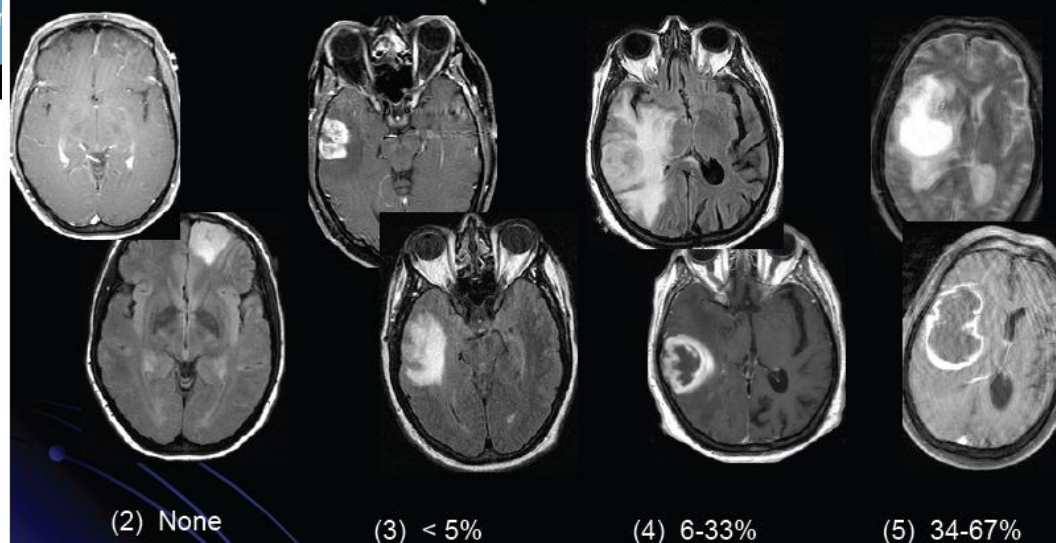
# VASARI Feature Set

## f5 – Proportion Enhancing



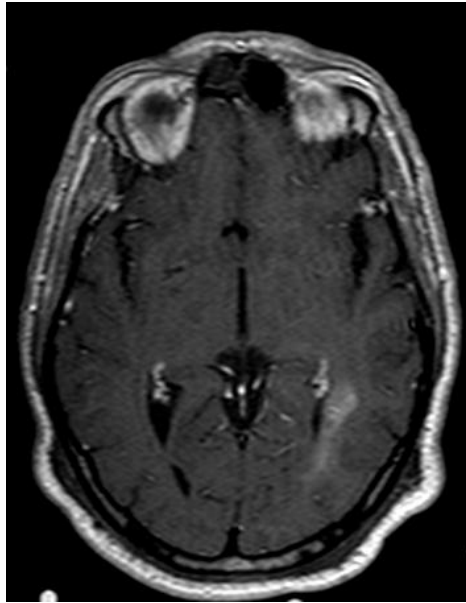
Visually, when scanning through the entire tumor volume, what proportion of tumor would you estimate is **enhancing**. (Assuming that the entire abnormality is comprised of: (1) an enhancing component, (2) a non-enhancing component and (4) a edema component.)

## f7 – Proportion Necrosis



Visually, when scanning through the entire tumor volume, what proportion of the tumor is estimated to represent necrosis. Necrosis is defined as a region within the tumor that does not enhance or shows markedly diminished enhancement, is high on T2W and proton density images, is low on T1W images, and has an irregular border). (Assuming that the entire abnormality may be comprised of: (1) an enhancing component, (2) a non-enhancing component, (3) a necrotic component and (4) a edema component.)

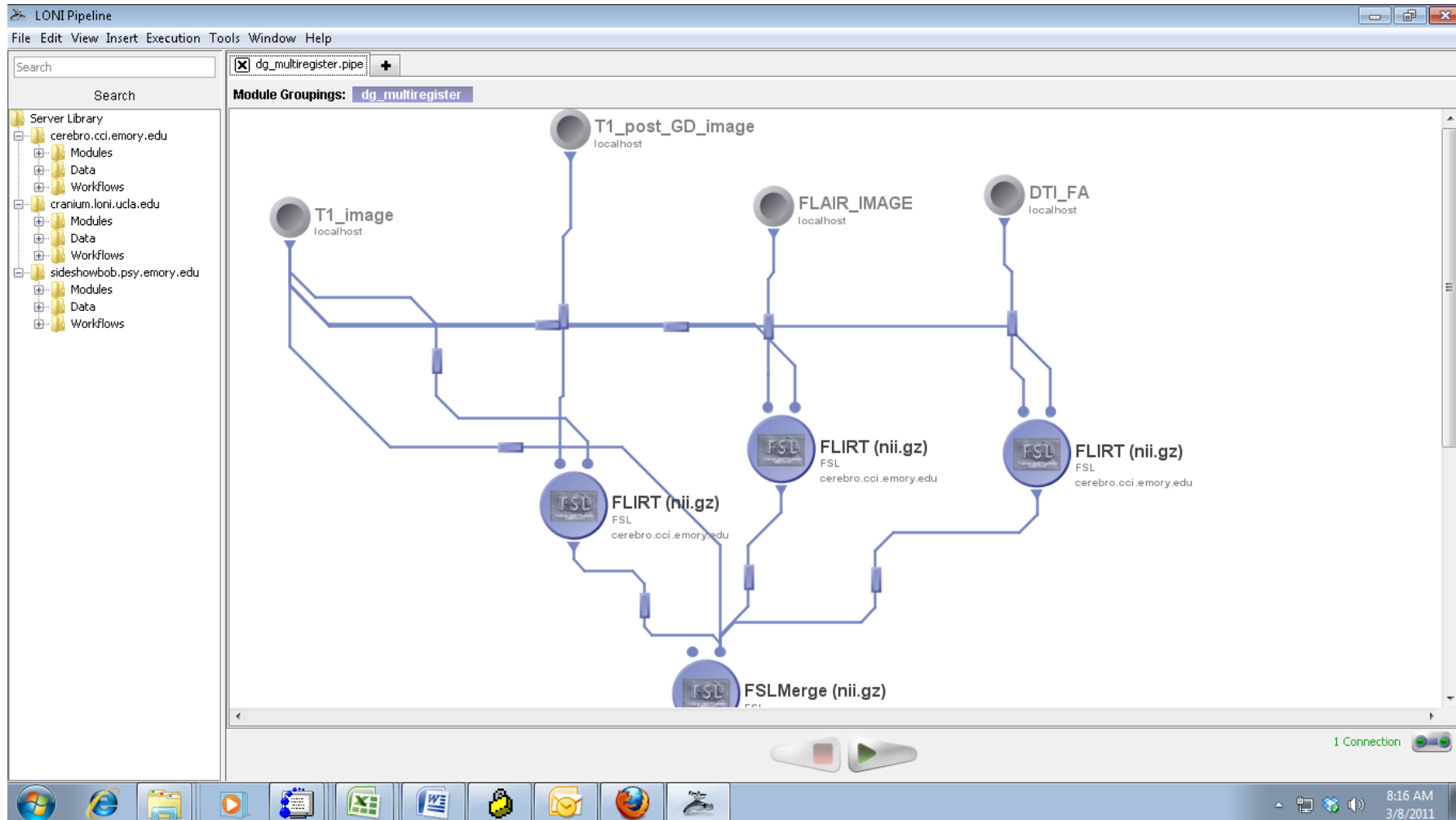
# Molecular and Pathologic Correlates of MR Features



**MRI of 75 TCGA GBMs reviewed by 3 neuroradiologists using VASARI feature set**

**MR Features compared to TCGA Neuropathology Classes, Transcriptional Classes, Genetic Alterations**

# Automated feature extraction pipeline also being developed for MRI





notes:

Basically the descriptions are often duplicated or nonsensical-- to parse this we need to manually tag the sequences from within a given MRI session

Scans

Scan	Type	Usability	Files	Note
+ 1	SAG LOCAL	usable	Show Counts	
+ 2	AXIAL FSE	usable	Show Counts	
+ 3	AXIAL T2 FLAIR	usable	Show Counts	
+ 4	DWI MAP	usable	Show Counts	
+ 5	AXIAL T1 PRE GD	usable	Show Counts	
+ 6	AXIAL GRE	usable	Show Counts	
+ 7	AXIAL T1 PRE GD	usable	Show Counts	
+ 8	NEW AXIAL PERFUSION/20S DELAY	usable	Show Counts	
- 9	AXIAL T1 POST GD	usable	Show Counts	

Image

